

2/20 O/PE

Serial Number:

09/900,425A

CRF Processing Date:

2/28/2002

Edited by:

Verified by:

(STIC staff)

ENTERED

☐

Changed a file from non-ASCII to ASCII

☐

Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐

Edited a format error in the Current Application Data section, specifically:

☐

Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____

☐

Added the mandatory heading and subheadings for "Current Application Data".

☐

Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐

Changed the spelling of a mandatory field (the headings or subheadings), specifically:

☐

Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

☐

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

☐

Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐

Inserted colons after headings/subheadings. Headings edited included:

☐

Deleted extra, invalid, headings used by an applicant, specifically:

☒

Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____

☐

Inserted mandatory headings, specifically: _____

☐

Corrected an obvious error in the response, specifically: _____

☐

Edited identifiers where upper case is used but lower case is required, or vice versa.

☐

Corrected an error in the Number of Sequences field, specifically: _____

☐

A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐

Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐

Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/900,425A DATE: 02/28/2002
TIME: 19:06:20

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\02282002\I900425A.raw

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3 <110> APPLICANT: Wu, Hongjiang
4   Crooke, Stanley T.
6 <120> TITLE OF INVENTION: Human RNase III and Compositions and Uses Thereof
8 <130> FILE REFERENCE: ISPH-0522
W--> 9 <140> CURRENT APPLICATION NUMBER: US 09/900,425A
C--> 10 <141> CURRENT FILING DATE: 2002-01-29
12 <150> PRIOR APPLICATION NUMBER: US 09/479,783
13 <151> PRIOR FILING DATE: 2000-01-07
15 <150> PRIOR APPLICATION NUMBER: US 08/870,608
16 <151> PRIOR FILING DATE: 1997-06-06
18 <150> PRIOR APPLICATION NUMBER: US 08/659,440
19 <151> PRIOR FILING DATE: 1996-06-06
21 <160> NUMBER OF SEQ ID NOS: 36
23 <170> SOFTWARE: PatentIn version 3.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 4764
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
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35 cccatatcat caaggagctg ataatctagt ggaagagtta gacgtgtgca tacttcaacta    180
37 tgatatgagg cagtctctga gcttatattc tctgtggaag atgtgacata tccaggcgga    240
39 acatcatgat gcagggaac acatgtcaca gaatgtcgtt ccaccggga cgagggtgtc    300
41 cccgaggacg aggaggacat ggagccagac cctcagcacc atcctttagg ccccaaaatc    360
43 tgaggctgct tcaccctcag cagcctcctg tgcaatatca atatgaacct ccaagtgcc    420
45 ctccaccac tttctcaaac tctccagccc ccaattttct cctccacga ccagactttg    480
47 tacccttccc cccacccatg cctccgtcag cgcaaggccc tottcccccc tgcccaatca    540
49 ggcgccttt ccccaaccac cagatgaggc accccttccc agttcctcct tgttttctc    600
51 ccatgccacc accaatgcct tgtcctaata acccccagc cctggggca cctcctggac    660
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55 tcatgccgca gcaggttaat tatcagtacc ctccgggcta ttctcaccac aacttcccac    780
57 ctcccagttt taatagtttc cagaacaacc ctagtctttt cctgcccagt gctaataaca    840
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61 gaaggtcccc agaaaggctg aaacactatg atgaccacag gcaccgagat cacagtcattg    960
63 ggcgaggtga gaggcacggg tccctggatc ggcgggagcg aggcgcagc cccgacagga    1020
65 gaagacaaga cagccggtac agatctgatt atgaccgagg gagaacacca tctcgcacc    1080
67 gcagctacga acggagcaga gagcgagaac gggagagaca caggcatcga gacaaccgaa    1140
69 gatcaccatc tctggaaagg tcctacaaaa aagagtataa gagatctgga aggagttacg    1200
71 gtttatcggt tgttcctgaa cctgctggat gcacaccaga attacctggg gagattatta    1260
73 aaaatacaga ttcttgggccc ccacccctgg agattgtgaa tcatcgctcc ccaagtaggg    1320
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79 agaattgagga ggaagaagaa gaacttctta agcctgtgtg gattcgatgc actcattcag 1500
81 aaaactacta ctccagtgc cccatggatc aggtgggaga ttctacagt gttggaacga 1560
83 gtaggcttcg tgacttatat gacaaatttg aggaggagtt ggggagcagg caagaaaagg 1620
85 ccaaagctgc tcggcctccg tgggaacctc caaagacgaa gctcgatgaa gatttagaga 1680
87 gttccagtga atccgagtgt gagtctgatg aggacagcac ctgttctagc agctcagact 1740
89 ctgaagtgtt tgacgttatt gcagaaatca aacgcaaaaa ggcccacctc gaccgacttc 1800
91 atgatgaact ttggtacaac gatccaggcc agatgaatga tggaccactc tgcaaatgca 1860
93 gcgcaaaggc aagacgcaca ggaattaggc acagcattta tcctggagaa gaggccatca 1920
95 agccctgtcg tcctatgacc aacaatgctg gcagactttt ccactaccgg atcacagtct 1980
97 ccccgctac gaacttttta actgacaggc caactgttat agaatacgat gatcacgagt 2040
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107 ttcatthcat gccacgtttt gtaagatttc ttccagatgg aggaaaggaa gtgctgtcca 2340
109 tgcaccagat tctcctgtac ttgttaaggt gcagcaaagc cctggtgcct gaggaggaga 2400
111 ttgccaatat gcttcagtgg gaggagctgg agtggcagaa atatgcagaa gaatgcaaaag 2460
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117 ctgcacagtt gagttatgca ggagaccac agtaccaaaa actgtggaag agttatgtga 2640
119 aacttcgcca cctcctagca aatagtccca aagtcaaaa aactgacaaa cagaagctgg 2700
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141 atccatttat gctgtatgct cacgggcctg acctttgtag agaatcggac cttcgacatg 3360
143 caatggccaa ttgttttgaa gcgttaatag gagctgttta cttggaggga agcctggagg 3420
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149 aaacttctcc agttctacaa aaacttactg agtttgaaga agcaattgga gtaattttta 3600
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171 aagcggaaat gggagcagca atggatgcgc ttgaaaaata taattttccc cagatggccc 4260
173 atcagaagcg gttcatcgaa cggaagtaca gacaagagtt aaaagaaatg aggtgggaaa 4320
175 gagagcatca agagagagag ccagatgaga ctgaagacat caagaaataa aggagggcac 4380

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179 agttttcctg cagacaatga acgaagtgtg ctcatgaaa taaaatacag agtcaaatcg 4500
181 ctattgttgt tttaatgata tgtttttagc tggatggtct ttattacaaa gtattagatt 4560
183 tttcttctat ttaacggaaa acttgacttt ggtgaatgtg cattacttcc ttttattttg 4620
185 ctcttttaaat aataaaattc aagaagcata ttctatgtgg aatagatcct gtttttccat 4680
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189 taaaaaaaaa aaaaaaaaaa aaaa 4764
192 <210> SEQ ID NO: 2
193 <211> LENGTH: 1374
194 <212> TYPE: PRT
195 <213> ORGANISM: Homo sapiens
197 <400> SEQUENCE: 2
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200 1 5 10 15
202 Gly Cys Pro Arg Gly Arg Gly Gly His Gly Ala Arg Pro Ser Ala Pro
203 20 25 30
205 Ser Phe Arg Pro Gln Asn Leu Arg Leu Leu His Pro Gln Gln Pro Pro
206 35 40 45
208 Val Gln Tyr Gln Tyr Glu Pro Pro Ser Ala Pro Ser Thr Thr Phe Ser
209 50 55 60
211 Asn Ser Pro Ala Pro Asn Phe Leu Pro Pro Arg Pro Asp Phe Val Pro
212 65 70 75 80
214 Phe Pro Pro Pro Met Pro Pro Ser Ala Gln Gly Pro Leu Pro Pro Cys
215 85 90 95
217 Pro Ile Arg Pro Pro Phe Pro Asn His Gln Met Arg His Pro Phe Pro
218 100 105 110
220 Val Pro Pro Cys Phe Pro Pro Met Pro Pro Pro Met Pro Cys Pro Asn
221 115 120 125
223 Asn Pro Pro Val Pro Gly Ala Pro Pro Gly Gln Gly Thr Phe Pro Phe
224 130 135 140
226 Met Met Pro Pro Pro Ser Met Pro His Pro Pro Pro Pro Pro Val Met
227 145 150 155 160
229 Pro Gln Gln Val Asn Tyr Gln Tyr Pro Pro Gly Tyr Ser His His Asn
230 165 170 175
232 Phe Pro Pro Pro Ser Phe Asn Ser Phe Gln Asn Asn Pro Ser Ser Phe
233 180 185 190
235 Leu Pro Ser Ala Asn Asn Ser Ser Ser Pro His Phe Arg His Leu Pro
236 195 200 205
238 Pro Tyr Pro Leu Pro Lys Ala Pro Ser Glu Arg Arg Ser Pro Glu Arg
239 210 215 220
241 Leu Lys His Tyr Asp Asp His Arg His Arg Asp His Ser His Gly Arg
242 225 230 235 240
244 Gly Glu Arg His Arg Ser Leu Asp Arg Arg Glu Arg Gly Arg Ser Pro
245 245 250 255
247 Asp Arg Arg Arg Gln Asp Ser Arg Tyr Arg Ser Asp Tyr Asp Arg Gly
248 260 265 270
250 Arg Thr Pro Ser Arg His Arg Ser Tyr Glu Arg Ser Arg Glu Arg Glu
251 275 280 285
253 Arg Glu Arg His Arg His Arg Asp Asn Arg Arg Ser Pro Ser Leu Glu

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254      290      295      300
256 Arg Ser Tyr Lys Lys Glu Tyr Lys Arg Ser Gly Arg Ser Tyr Gly Leu
257 305      310      315      320
259 Ser Val Val Pro Glu Pro Ala Gly Cys Thr Pro Glu Leu Pro Gly Glu
260      325      330      335
262 Ile Ile Lys Asn Thr Asp Ser Trp Ala Pro Pro Leu Glu Ile Val Asn
263      340      345      350
265 His Arg Ser Pro Ser Arg Glu Lys Lys Arg Ala Arg Trp Glu Glu Glu
266      355      360      365
268 Lys Asp Arg Trp Ser Asp Asn Gln Ser Ser Gly Lys Asp Lys Asn Tyr
269      370      375      380
271 Thr Ser Ile Lys Glu Lys Glu Pro Glu Glu Thr Met Pro Asp Lys Asn
272 385      390      395      400
274 Glu Glu Glu Glu Glu Glu Leu Leu Lys Pro Val Trp Ile Arg Cys Thr
275      405      410      415
277 His Ser Glu Asn Tyr Tyr Ser Ser Asp Pro Met Asp Gln Val Gly Asp
278      420      425      430
280 Ser Thr Val Val Gly Thr Ser Arg Leu Arg Asp Leu Tyr Asp Lys Phe
281      435      440      445
283 Glu Glu Glu Leu Gly Ser Arg Gln Glu Lys Ala Lys Ala Ala Arg Pro
284      450      455      460
286 Pro Trp Glu Pro Pro Lys Thr Lys Leu Asp Glu Asp Leu Glu Ser Ser
287 465      470      475      480
289 Ser Glu Ser Glu Cys Glu Ser Asp Glu Asp Ser Thr Cys Ser Ser Ser
290      485      490      495
292 Ser Asp Ser Glu Val Phe Asp Val Ile Ala Glu Ile Lys Arg Lys Lys
293      500      505      510
295 Ala His Pro Asp Arg Leu His Asp Glu Leu Trp Tyr Asn Asp Pro Gly
296      515      520      525
298 Gln Met Asn Asp Gly Pro Leu Cys Lys Cys Ser Ala Lys Ala Arg Arg
299      530      535      540
301 Thr Gly Ile Arg His Ser Ile Tyr Pro Gly Glu Glu Ala Ile Lys Pro
302 545      550      555      560
304 Cys Arg Pro Met Thr Asn Asn Ala Gly Arg Leu Phe His Tyr Arg Ile
305      565      570      575
307 Thr Val Ser Pro Pro Thr Asn Phe Leu Thr Asp Arg Pro Thr Val Ile
308      580      585      590
310 Glu Tyr Asp Asp His Glu Tyr Ile Phe Glu Gly Phe Ser Met Phe Ala
311      595      600      605
313 His Ala Pro Leu Thr Asn Ile Pro Leu Cys Lys Val Ile Arg Phe Asn
314      610      615      620
316 Ile Asp Tyr Thr Ile His Phe Ile Glu Glu Met Met Pro Glu Asn Phe
317 625      630      635      640
319 Cys Val Lys Gly Leu Glu Leu Phe Ser Leu Phe Leu Phe Arg Asp Ile
320      645      650      655
322 Leu Glu Leu Tyr Asp Trp Asn Leu Lys Gly Pro Leu Phe Glu Asp Ser
323      660      665      670
325 Pro Pro Cys Cys Pro Arg Phe His Phe Met Pro Arg Phe Val Arg Phe
326      675      680      685

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Input Set : A:\PTO.AMC.txt

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328 Leu Pro Asp Gly Gly Lys Glu Val Leu Ser Met His Gln Ile Leu Leu
329      690                      695                      700
331 Tyr Leu Leu Arg Cys Ser Lys Ala Leu Val Pro Glu Glu Glu Ile Ala
332 705                      710                      715                      720
334 Asn Met Leu Gln Trp Glu Glu Leu Glu Trp Gln Lys Tyr Ala Glu Glu
335                      725                      730                      735
337 Cys Lys Gly Met Ile Val Thr Asn Pro Gly Thr Lys Pro Ser Ser Val
338                      740                      745                      750
340 Arg Ile Asp Gln Leu Asp Arg Glu Gln Phe Asn Pro Asp Val Ile Thr
341                      755                      760                      765
343 Phe Pro Ile Ile Val His Phe Gly Ile Arg Pro Ala Gln Leu Ser Tyr
344                      770                      775                      780
346 Ala Gly Asp Pro Gln Tyr Gln Lys Leu Trp Lys Ser Tyr Val Lys Leu
347 785                      790                      795                      800
349 Arg His Leu Leu Ala Asn Ser Pro Lys Val Lys Gln Thr Asp Lys Gln
350                      805                      810                      815
352 Lys Leu Ala Gln Arg Glu Glu Ala Leu Gln Lys Ile Arg Gln Lys Asn
353                      820                      825                      830
355 Thr Met Arg Arg Glu Val Thr Val Glu Leu Ser Ser Gln Gly Phe Trp
356                      835                      840                      845
358 Lys Thr Gly Ile Arg Ser Asp Val Cys Gln His Ala Met Met Leu Pro
359                      850                      855                      860
361 Val Leu Thr His His Ile Arg Tyr His Gln Cys Leu Met His Leu Asp
362 865                      870                      875                      880
364 Lys Leu Ile Gly Tyr Thr Phe Gln Asp Arg Cys Leu Leu Gln Leu Ala
365                      885                      890                      895
367 Met Thr His Pro Ser His His Leu Asn Phe Gly Met Asn Pro Asp His
368                      900                      905                      910
370 Ala Arg Asn Ser Leu Ser Asn Cys Gly Ile Arg Gln Pro Lys Tyr Gly
371                      915                      920                      925
373 Asp Arg Lys Val His His Met His Met Arg Lys Lys Gly Ile Asn Thr
374                      930                      935                      940
376 Leu Ile Asn Ile Met Ser Arg Leu Gly Gln Asp Asp Pro Thr Pro Ser
377 945                      950                      955                      960
379 Arg Ile Asn His Asn Glu Arg Leu Glu Phe Leu Gly Asp Ala Val Val
380                      965                      970                      975
382 Glu Phe Leu Thr Ser Val His Leu Tyr Tyr Leu Phe Pro Ser Leu Glu
383                      980                      985                      990
385 Glu Gly Gly Leu Ala Thr Tyr Arg Thr Ala Ile Val Gln Asn Gln His
386                      995                      1000                      1005
388 Leu Ala Met Leu Ala Lys Lys Leu Glu Leu Asp Pro Phe Met Leu Tyr
389                      1010                      1015                      1020
391 Ala His Gly Pro Asp Leu Cys Arg Glu Ser Asp Leu Arg His Ala Met
392 1025                      1030                      1035                      1040
394 Ala Asn Cys Phe Glu Ala Leu Ile Gly Ala Val Tyr Leu Glu Gly Ser
395                      1045                      1050                      1055
397 Leu Glu Glu Ala Lys Gln Leu Phe Gly Arg Leu Leu Phe Asn Asp Pro
398                      1060                      1065                      1070
400 Asp Leu Arg Glu Val Trp Leu Asn Tyr Pro Leu His Pro Leu Gln Leu

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 02/28/2002
PATENT APPLICATION: US/09/900,425A TIME: 19:06:21

Input Set : A:\PTO.AMC.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:2; Line(s) 419